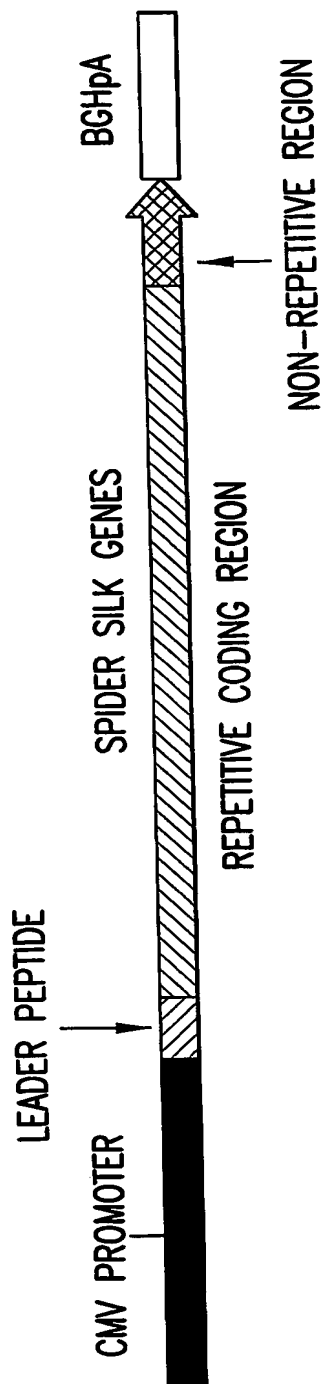


1/10

DNA EXPRESSION CONSTRUCTS USED TO PRODUCE RC-DRAGLINE SPIDER SILKS IN MAMMALIAN CELLS.



SPIDER SILK GENES EXPRESSED	cDNA SIZE (kb)	NON-REPETITIVE 3' -END (kb)	"TAG"	PREDICTED RC-SPIDER SILK SIZE	
				# AMINO ACIDS	kD
ADF-3 His	1.7	0.3	myc, His(8)	677	63
ADF-3	1.7	"	-	652	60
ADF-33	3.4	"	-	1090	110
ADF-333	4.7	"	-	1568	140
MaSpII	1.6	"	-	658	59
MaSpI	1.9	"	-	719	59
MaSpI(2)	3.6	"	-	1316	106

FIG.1

2/10

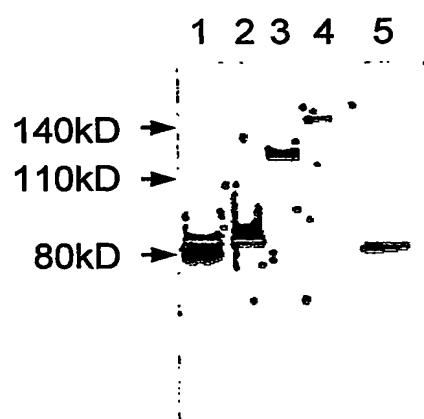


FIG. 2A

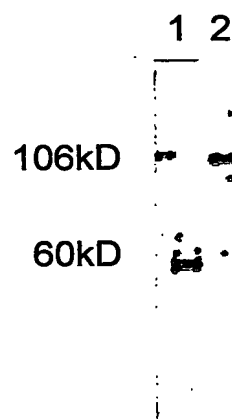


FIG. 2B

3/10

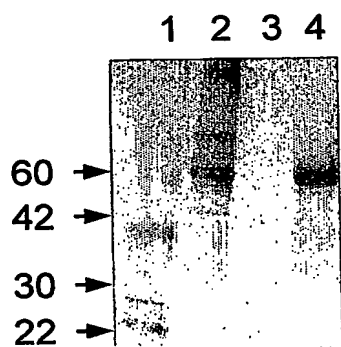


FIG.3A

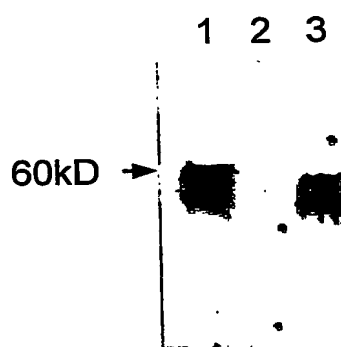


FIG.3B

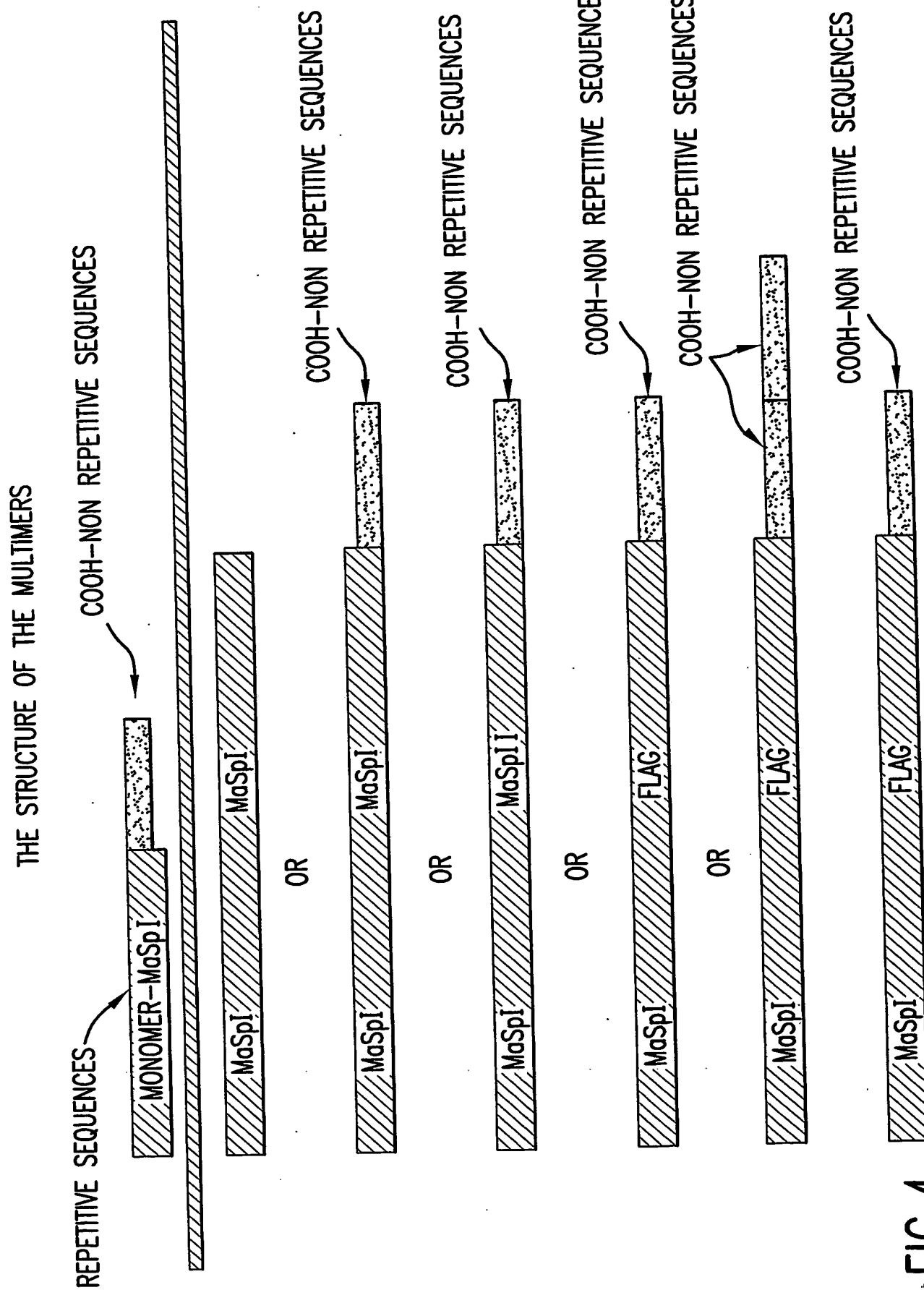


FIG. 4

5/10

SEQ	MoSp1_Translation (M4)	
KEYWORD	PROTEIN	
ORIGIN		
QGAGAAAAAA	GGAGQGGYGG	LGSQGAGRGG
QGAGAAAAAA	GGAGQGGYGG	LGSQGAGRGGGLGG
QGAGAAAAAA	GGVCGGG	LGGQGAG
QGAGAAAAAA	GGAGQGGYGG	LGSQGAGRGGSGG
QGAGAAAAAA	GGAGQGGYGG	LGSQGAGRGGGLGG
QGAGAAAAAA	GGAGQGGYGG	LGGQGAGQGGYGG LGSQGAGRGGGLGG
QGAGAAAAAA	GGAGQGG	LGGQGAG
QGAGAAAAAA	GGAGQGGYGG	LGSQGAGRGG
QGAGAAAAAA	VGAGQGGYGGQGAGQGGYGG	LGSQGAGRGGGLGG
QGAGAAAAAA	GGAGQGG	LGGQGAG
QGAGAAAAAA	GGAGQGGYGG	LGNQGAGRGG
QAAAAAAGGA	GGAGYGG	LGSQGAGRGGGLGG
QGAGAAAAAA	GGAGQGGYGG	LGGQGAGQGGYGG LGSQSGRGGGLGG
QGAGAAAAAA	GGAGQGG	LGGQGAG
QGAGAAAAAA	GGVRQGGYGG	LGSQGAGRGG
QGAGAAAAAA	GGAGQGGYGG	LGGQGVGRGG LGG
QGAGAAAA	GGAGQGGYGG	
VSGASAASAAASRLSSPQASSRVSSAVSNL VASGPTNSAAL SST I SNVVSQIGASNPGLSGCDVL IQALLEVVSAL I		
QILGSSSIGQVNYGSAGQATQIVGQSVYQAL		

FIG.5

6/10

SEQ	MoSp2_Translation		
KEYWORD	PROTEIN		
ORIGIN			
	PGGYGPGQQGPGGYGPGQQGP	SGPGS	AAAAAAAAAA
	GPGGYGPGQQGPGGYGPGQQGPGRYGPGQQGP	SGPGS	AAAAAA
	GSGQQGPGGYGPRQQGPGGYGQQQQGP	SGPGS	AAAASAAASA
	ESGQQGPGGYGPGQQGPGGYGPGQQGPGGYGPGQQGP	SGPGS	AAAAAAAA
	SGPGQQGPGGYGPGQQGPGGYGPGQQGP	SGPGS	AAAAAAAA
	SGPGQQGPGGYGPGQQGPGGYGPGQQGL	SGPGS	AAAAAA
	GPGQQGPGGYGPGQQGP	SGPGS	AAAAAAAA
	GPGGYGPGQQGPGGYGPGQQGP	SGAGS	AAAAAA
	GPGQQGLGGYGPGQQGPGGYGPGQQGPGGY	GPGS	ASAAAAAA
	GPGQQGPGGYGPGQQGP	SGPGS	ASAAAAAA
	GPGGYGPGQQGPGGYAPGQQGP	SGPGS	ASAAAAAA
	GPGGYGPGQQGPGGYAPGQQGP	SGPGS	AAAAAAAA
	GPGGYGPAQQGP	SGPGI	AASAASA
	GPGGYGPAQQGPAGY	GPGS	AVAASAGAGSA
	GYGPGSQASAAASRLASPDGARVASAVSNLVSSGPTSSAALSSVINSNAVSQIGASNPGLSGCDVL IQALLE IVSACV		
	TILSSSSIGQVNYGAASQFAQVVGQSVLSAF		

FIG.6

7/10

Translation of AdfS (1-3410)

Universal code

Total amino acid number: .1130, MW-115213

Max ORF: 1-3270, 1090 AA, MW-110427

adf-3 TRANSLATION

ARA

	GSGQQGPGQQGPGQQGPGQQGP	YGP
ASAAAAA	GGYGP GSGQQGPSQQGPGQQGP	YGP
ASAAAAA	GGYGP GSGQQGPGGQGP	YGP
SSAAAAA	GGNGP GSGQQGAGQQGPGQQGPG	
ASAAAAA	GGYGP GSGQQGPGQQGPGGQGP	YGP
ASAAAAA	GGYGP GSGQ-GPGQQGPGGQGP	YGP
ASAAAAA	GGYGP GSGQQGPGQQGPGQQGP	YGP
ASAAAAA	GGYGP GYGQQGPGQQGPGGQGP	YGP
ASAASAAS	GGYGP GSGQQGPGQQGPGGQGP	YGP
ASAAAAA	GGYGP GSGQQGPGQQGPGQQGPGQQGPGGQGP	YGP
ASAAAAA	GGYGP GSGQQGPGQQGPGQQGP	YGP
ASAAAGAA	GGYGP GSGQQGPGQQGPGQQGP	YGP
ASAAAAA	GQQGPGQQGPGQQGPGGQGR	YGP
AASAASV	GGYGP G	
SSVPVASAVASRLSSPAASSRVSSAVSSLVSSGPTKHALLSNTISSVVSQVSASNPGLSGCDVLVQALLEVVSALVSI		
LGSSSIGQINYGASAQYTQMVGSVAQALA		

FIG.7

8/10

Translation of ADF-1

Fibroin (Araneus diadematus clone ADF-1 C-terminal fragment)

```
SEQ      1 HESSYAAAMA ASTRNSDFIR NMSYQMGRLL SNAGAITEST ASSAASSASS
          51 TVTESIRTYG PAAIFSGAGA GAGVGVGGAG GYGQGYGAGA GAGAGAGAGA
        101 GGAGGYGQGY GAGAAAAAGA GAGAAGGYGG GSGAGAGGAG GYGQGYGAGS
          151 GAGAGAAAAA GASAGAAGGY GGGAGVGAGA GAGAAGGYGQ SYGSGAGAGA
          201 GAGAAAAAGA GARAAGGYGG GYGAGAGAGA GAAASAGASG GYGGGYGGGA
          251 GAGAVAGASA GSYGGAVNRL SSAGAASRVS SNVAAIASAG AAALPNVISN
          301 IYSGVLSSGV SSSEALIQAL LEVISALIHV LGSASIGNVS SVGVNSALNA
          351 VQNAVGayAG
```

FIG.8

9/10

Translation of ADF-2

Fibroin (Araneus diadematus clone ADF-2 C-terminal fragment) (9CI)(CA
INDEX NAME)

```
SEQ      1  GSQGAGGAGQ GGYGAGGGGA AAAAAA AVGA GGGGQGGLGS GGAGQGYGAG
      51  LGGQGGASAA AAAAGGQGGQ GGQGGYGGLG SQGAGGAGQL GYGAGQESAA
     101  AAAAAAGGAG GGGQGGLGAG GAGQGYGAAG LGGQGGAGQG GGSGAAAAAG
     151  GQGQGGGYGG LGPQGAGGAG QGGYGGGSLQ YGGQQAQAA AASAAASRLS
     201  SPSAAARVSS AVSLVSNGGP TSPAALSSSI SNVVSQISAS NPGLSGCDIL
     251  VQALLEIISA LVHILGSANI GPNSSSAGQ SASIVGQSVY RALS
```

FIG.9

10/10

Translation of ADF-4

Fibroin (Araneus diadematus clone ADF-4 C-terminal fragment) (9CI) (CA
INDEX NAME)

```
SEQ      1  AGSSAAAAAA ASGSGGYGPE NQGPGSPVAY GPGGPVSSAA AAAAAGSGPG
      51  GYGPENQGPS GPGGYGPGGS GSSAAAAAAA ASGPGGYGPG SQGPSGPGGS
     101  GGYGPGSQGA SGPGGPGASA AAAAAAAAAS GPGGYGPGSQ GPSGPGAYGP
     151  GGPSSAAAA AAAASGPGGY GPGSQGPSGP GVGPGGPGS SAAAAAAGS
     201  GPGGYGPENQ GPSGPGGYGP GSGSSAAAA AAAASGPGGY GPGSQGPSGP
     251  GSGGYGPGS QGSGPGGASA AAAAAAASGP GGYGPGSQGP SGPGYQGPGS
     301  PGAYGPSPSA SASVAASVYL RLQPRLEVSS AVSSLVSSGP TNGAAVSGAL
     351  NSLVSQISAS NPGLSGCDAL VQALLELVSA LVAILSSASI GQVNVSSVSQ
     401  STQMISQALS
```

FIG.10